

Serial No.: 09/745,965
Attorney Docket: 3373.1

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (currently amended) A computer implemented method for selecting nucleic acid probes comprising:

inputting quality scores and locations for a plurality (n) of candidate probes;

selecting k number of probes from the n number of candidate probes, wherein the selected probes have a maximum aggregate adjusted quality score; wherein the adjusted quality score is based upon the quality score and the overlapping of the selected probes.
2. (currently amended) The method of Claim 1 wherein the adjusted quality score is calculated according to: $S' = S \sqrt{\frac{l-o}{l}}$, wherein S' is an adjusted quality score; S is a the initial quality score; l is the probe length, and o is the overlap the probe has with other probes.
3. (canceled)
4. (currently amended) The method of ~~Claim 3~~ Claim 2 wherein k is greater than 3.
5. (original) The method of Claim 4 wherein k is greater than 5.
6. (original) The method of Claim 5 wherein k is greater than 10.

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7. (original) The method of Claim 6 wherein k is greater than 15.
8. (currently amended) The method of Claim 2 wherein the selecting step comprises performing dynamic programming optimization on the n number of candidate probes to adjust their quality scores to the extent of overlap between them to obtain an optimal k number of probes with optimal aggregate adjusted quality scores.
9. (currently amended) The method of Claim 8 wherein the selecting comprises steps of:
 - calculating best adjusted quality scores ($Score(i, t)$) for probe i last with $t-1$ probes chosen before i and previous location j providing this best score ($Last(i, k)$);
 - determining the best adjusted quality scores for $Score(j, k)$ to select the last probe; and
 - selecting the next probe according to $Last$ (the probe selected, number of probes remaining to be selected); and
 - repeating the selecting step until all k probes are selected.
10. (original) A system for selecting nucleic acid probes comprising:
 - a processor; and

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a memory coupled with the processor, the memory storing a plurality of machine instructions that cause the processor to perform logical steps, wherein the logical steps include:

inputting quality scores and locations for a plurality (n) of candidate probes;
selecting k number of probes from the n number of candidate probes, wherein the selected probes have a maximum aggregate adjusted quality score; wherein the adjusted quality score is based upon the quality score and the overlapping of the selected probes.

11. (original) The system of Claim 10 wherein the adjusted quality score is calculated

according to: $S' = S \sqrt{\frac{l-o}{l}}$, wherein S' is an adjusted quality score; S is a quality score; l is the probe length, o is the overlap the probe has with other probes.

12. (canceled)

13. (currently amended) The system of Claim 11 wherein k is greater than 3.

14. (original) The system of Claim 13 wherein k is greater than 5.

15. (original) The system of Claim 14 wherein k is greater than 10.

16. (original) The system of Claim 15 wherein k is greater than 15.

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17. (currently amended) The system of Claim 16 wherein the selecting step comprises performing dynamic programming optimization on the n number of candidate probes to adjust their quality scores to the extent of overlap between them to obtain an optimal k number of probes with optimal aggregate adjusted quality scores.
18. (original) The system of Claim 17 wherein the selecting comprises steps of:
- calculating best adjusted quality scores ($Score(i, t)$) for probe i last with $t-1$ probes chosen before i and previous location j providing this best score ($Last(i, k)$);
 - determining the best adjusted quality scores for $Score(j, k)$ to select the last probe; and
 - selecting the next probe according to $Last$ (the probe selected, number of probes remain to be selected); and
 - repeating the selecting step until all k probes are selected.
19. (original) A computer readable medium having computer executable instructions for performing a method comprising:
- inputting quality scores and locations for a plurality (n) of candidate probes;
 - selecting k number of probes from the n number of candidate probes, wherein the selected probes have a maximum aggregate adjusted quality score;

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wherein the adjusted quality score is based upon the quality score and the overlapping of the selected probes.

20. (original) The computer readable medium of Claim 19 wherein the adjusted

quality score is calculated according to: $S' = S \sqrt{\frac{(l-o)}{l}}$, wherein S' is an adjusted quality score; S is a quality score; l is the probe length, o is the overlap the probe has with other probes.

21. (canceled)

22. (currently amended) The computer readable medium of ~~Claim 21~~ Claim 20 wherein k is greater than 3.

23. (original) The computer readable medium of Claim 22 wherein k is greater than 5.

24. (original) The computer readable medium of Claim 23 wherein k is greater than 10.

25. (original) The computer readable medium of Claim 24 wherein k is greater than 15.

26. (currently amended) The computer readable medium of Claim 25 wherein the selecting step comprises performing dynamic programming optimization on the n

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number of candidate probes to adjust their quality scores to the extent of overlap between them to obtain an optimal k number of probes with optimal aggregate adjusted quality scores.

27. (original) The computer readable medium of Claim 26 wherein the selecting comprises steps of:

calculating best adjusted quality scores ($Score(i, t)$) for probe i last with $t-1$ probes chosen before i and previous location j providing this best score ($Last(i, k)$);

determining the best adjusted quality scores for $Score(j, k)$ to select the last probe; and

selecting the next probe according to $Last$ (the probe selected, number of probes remain to be selected); and

repeating the selecting step until all k probes are selected.